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RAW SEQUENCE LISTING

DATE: 08/17/2001

PATENT APPLICATION: US/09/756,071B

TIME: 14:25:18

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\08172001\I756071B.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Tryggvason, Karl
6 Kallunki, Pekka
7 Pyke, Charles
9 (ii) TITLE OF INVENTION: Laminin Chains: Diagnostic Uses
11 (iii) NUMBER OF SEQUENCES: 20
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
15 (B) STREET: 1100 Superior Ave, Suite 700
16 (C) CITY: Cleveland
17 (D) STATE: Ohio
18 (E) COUNTRY: USA
19 (F) ZIP: 44114
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/756,071B
C--> 29 (B) FILING DATE: 08-Jan-2001
35 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US 09/663,147
34 (B) FILING DATE: 150-September 2000
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Minnich, Richard, J.
39 (B) REGISTRATION NUMBER: 24,175
40 (C) REFERENCE/DOCKET NUMBER: TRV 20014
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 216-861-5582
44 (B) TELEFAX: 216-241-1666
46 (2) INFORMATION FOR SEQ ID NO: 1:
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 20 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
54 (ii) MOLECULE TYPE: other nucleic acid
55 (A) DESCRIPTION: /desc = "oligomer primers"
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
59 GGCTCACCAA GACTTACACA
61 (2) INFORMATION FOR SEQ ID NO: 2:
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 20 base pairs
65 (B) TYPE: nucleic acid

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66          (C) STRANDEDNESS: single
67          (D) TOPOLOGY: linear
69      (ii) MOLECULE TYPE: other nucleic acid
70          (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
74 GAATCACTGA GCAGCTGAAC                                     20
76 (2) INFORMATION FOR SEQ ID NO: 3:
78      (i) SEQUENCE CHARACTERISTICS:
79          (A) LENGTH: 20 base pairs
80          (B) TYPE: nucleic acid
81          (C) STRANDEDNESS: single
82          (D) TOPOLOGY: linear
84      (ii) MOLECULE TYPE: other nucleic acid
85          (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89 CAGTACCAGA ACCGAGTTCG                                     20
91 (2) INFORMATION FOR SEQ ID NO: 4:
93      (i) SEQUENCE CHARACTERISTICS:
94          (A) LENGTH: 20 base pairs
95          (B) TYPE: nucleic acid
96          (C) STRANDEDNESS: single
97          (D) TOPOLOGY: linear
99      (ii) MOLECULE TYPE: other nucleic acid
100          (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
102      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
104 CTGGTTACCA GGCTTGAGAG                                     20
106 (2) INFORMATION FOR SEQ ID NO: 5:
108      (i) SEQUENCE CHARACTERISTICS:
109          (A) LENGTH: 20 base pairs
110          (B) TYPE: nucleic acid
111          (C) STRANDEDNESS: single
112          (D) TOPOLOGY: linear
114      (ii) MOLECULE TYPE: other nucleic acid
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117      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
119 TTACTGCGGA ATCTCACAGC                                     20
121 (2) INFORMATION FOR SEQ ID NO: 6:
123      (i) SEQUENCE CHARACTERISTICS:
124          (A) LENGTH: 20 base pairs
125          (B) TYPE: nucleic acid
126          (C) STRANDEDNESS: single
127          (D) TOPOLOGY: linear
129      (ii) MOLECULE TYPE: other nucleic acid
130          (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
132      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
134 TACACTGTTC AACCCAGGGT                                     20
136 (2) INFORMATION FOR SEQ ID NO: 7:
138      (i) SEQUENCE CHARACTERISTICS:
139          (A) LENGTH: 20 base pairs

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140      (B) TYPE: nucleic acid
141      (C) STRANDEDNESS: single
142      (D) TOPOLOGY: linear
144      (ii) MOLECULE TYPE: other nucleic acid
145      (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
147      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
149 AAACAAGCCC TCTCACTGGT                                20
151 (2) INFORMATION FOR SEQ ID NO: 8:
153      (i) SEQUENCE CHARACTERISTICS:
154          (A) LENGTH: 20 base pairs
155          (B) TYPE: nucleic acid
156          (C) STRANDEDNESS: single
157          (D) TOPOLOGY: linear
159      (ii) MOLECULE TYPE: other nucleic acid
160      (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
162      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
164 GCGGAGACTG TGCTGATAAG                                20
166 (2) INFORMATION FOR SEQ ID NO: 9:
168      (i) SEQUENCE CHARACTERISTICS:
169          (A) LENGTH: 20 base pairs
170          (B) TYPE: nucleic acid
171          (C) STRANDEDNESS: single
172          (D) TOPOLOGY: linear
174      (ii) MOLECULE TYPE: other nucleic acid
175      (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
177      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
179 CATACCTCTC TACATGGCAT                                20
181 (2) INFORMATION FOR SEQ ID NO: 10:
183      (i) SEQUENCE CHARACTERISTICS:
184          (A) LENGTH: 20 base pairs
185          (B) TYPE: nucleic acid
186          (C) STRANDEDNESS: single
187          (D) TOPOLOGY: linear
189      (ii) MOLECULE TYPE: other nucleic acid
190      (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
192      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
194 AGTCTCGCTG AATCTCTCTT                                20
196 (2) INFORMATION FOR SEQ ID NO: 11:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 20 base pairs
200          (B) TYPE: nucleic acid
201          (C) STRANDEDNESS: single
202          (D) TOPOLOGY: linear
204      (ii) MOLECULE TYPE: other nucleic acid
205      (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
208      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
210 TTACAAC TAG CATGGTGCCC                                20
212 (2) INFORMATION FOR SEQ ID NO: 12:
214      (i) SEQUENCE CHARACTERISTICS:

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215      (A) LENGTH: 5200 base pairs
216      (B) TYPE: nucleic acid
217      (C) STRANDEDNESS: single
218      (D) TOPOLOGY: linear
220      (ii) MOLECULE TYPE: cDNA
223      (ix) FEATURE:
224          (A) NAME/KEY: sig_peptide
225          (B) LOCATION: 118..183
227      (ix) FEATURE:
228          (A) NAME/KEY: CDS
229          (B) LOCATION: 118..3699
231      (ix) FEATURE:
232          (A) NAME/KEY: polyA_site
233          (B) LOCATION: 4433
235      (ix) FEATURE:
236          (A) NAME/KEY: polyA_site
237          (B) LOCATION: 5195
240      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
242 GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG      60
244 AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCGG CACCGCC      117
246 ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG      165
247 Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
248   1           5           10           15
250 CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG      213
251 Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
252           20           25           30
254 AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT      261
255 Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
256           35           40           45
258 AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC      309
259 Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
260           50           55           60
262 TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC      357
263 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
264   65           70           75           80
266 TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT      405
267 Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
268           85           90           95
270 GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA      453
271 Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
272           100          105          110
274 TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC      501
275 Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
276           115          120          125
278 ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT      549
279 Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
280           130          135          140
282 GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT      597
283 Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala

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284	145		150		155		160	
286	GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG							645
287	Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu							
288		165		170		175		
290	GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT							693
291	Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His							
292		180		185		190		
295	TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC							741
296	Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr							
297		195		200		205		
299	TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT							789
300	Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn							
301		210		215		220		
303	GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT							837
304	Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe							
305	225		230		235		240	
307	AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA							885
308	Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys							
309		245		250		255		
311	TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC							933
312	Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp							
313		260		265		270		
315	TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC							981
316	Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile							
317		275		280		285		
319	CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC							1029
320	Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly							
321		290		295		300		
323	AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT							1077
324	Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn							
325	305		310		315		320	
327	GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT							1125
328	Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr							
329		325		330		335		
331	CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT							1173
332	Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr							
333		340		345		350		
336	GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC							1221
337	Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala							
338		355		360		365		
340	CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT							1269
341	Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys							
342		370		375		380		
344	CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC							1317
345	Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr							
346	385		390		395		400	
348	AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT							1365
349	Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys							
350		405		410		415		

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:890 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:894 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:970 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:978 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:982 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:1054 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14

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L:1062 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1066 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:1074 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14